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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2003, 05:10:54 ; Search time 1866 Seconds

(without alignments)  
9842.273 Million cell updates/sec

Title: US-10-091-628-1

Perfect score: 1134  
Sequence: 1 atgagagcattgtctccag.....acatcattcatggaatag 1134

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

ched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_estba:\*  
3: em\_estba:\*  
4: em\_estba:\*  
5: em\_estba:\*  
6: em\_estba:\*  
7: em\_estba:\*  
8: em\_estba:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_est6:\*  
15: em\_estfun:\*  
16: em\_estfun:\*  
17: gb\_est7:\*  
18: em\_estfun:\*  
19: em\_estfun:\*  
20: em\_estfun:\*  
21: em\_estfun:\*  
22: em\_estfun:\*  
23: em\_estfun:\*  
24: em\_estfun:\*  
25: em\_estfun:\*  
26: em\_estfun:\*  
27: em\_estfun:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	704.4	62.1	2125	11	AK018423	Mus muscu
2	450.4	39.7	652	10	BB613812	BB613812
3	335.4	29.6	972	12	BB613812	BB613812
4	327.4	28.9	356	10	BB613812	BB613812
5	200	17.6	658	10	BB625035	BB625035
6	200	17.6	662	10	BB664585	BB664585

7	194.2	17.1	642	9	AU176916	AU176916
8	189	16.7	760	13	BE168670	BE168670
9	184	16.2	274	10	BE151388	BE151388
10	182.6	16.1	543	17	AQ013853	AQ013853
11	162.6	14.5	538	10	BE030429	BE030429
12	162.4	14.3	686	10	AM107022	AM107022
13	149.4	13.2	666	10	BB625042	BB625042
14	142.2	12.5	919	13	BE149148	BE149148
15	141.2	12.5	876	10	BE234728	BE234728
16	140.4	12.4	307	10	BB605283	BB605283
17	140.4	12.4	419	10	BB846568	BB846568
18	138	12.2	628	10	BE031975	BE031975
19	137.6	12.1	803	9	BE1528386	BE1528386
20	137.4	12.1	928	12	BE236073	BE236073
21	136.8	12.0	632	10	BE218113	BE218113
22	136.4	12.0	404	10	AM786072	AM786072
23	136.4	11.7	846	13	BE144614	BE144614
24	131.4	11.6	799	13	BE1331108	BE1331108
25	130	11.5	476	9	BE1303923	BE1303923
26	128	11.3	410	9	BE1046372	BE1046372
27	127.2	11.2	860	13	BE1339089	BE1339089
28	123.8	10.9	511	13	BE180877	BE180877
29	121.4	10.7	668	10	BE439690	BE439690
30	119.8	10.6	904	9	BE1522530	BE1522530
31	107.6	9.5	615	14	BE155816	BE155816
32	105.8	9.3	465	17	BE1529753	BE1529753
33	104	9.2	404	9	BE1529753	BE1529753
34	103.4	9.1	974	12	BE235598	BE235598
35	103.2	9.1	1091	17	BE130380W	BE130380W
36	101.6	9.0	853	12	BE132464	BE132464
37	101.4	8.9	633	10	BE439637	BE439637
38	100.6	8.9	413	9	BE1066773	BE1066773
39	93.6	8.3	575	17	BE15290849	BE15290849
40	93.4	8.2	599	14	BE1529623	BE1529623
41	92	8.1	831	9	BE1530028	BE1530028
42	90.2	8.0	464	12	BE1043423	BE1043423
43	89.6	7.9	602	9	BE1119397	BE1119397
44	87	7.7	525	10	BE1668323	BE1668323
45	85.4	7.5	378	9	BE1386052	BE1386052

## ALIGNMENTS

RESULT 1	AK018423	2125 bp	linear	HTC 19-JAN-2002
LOCUS	AK018423			
DEFINITION	Mus musculus 16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430417G17; similar to ILEAL NA+-DEPENDENT BILE ACID TRANSPORTER (ISBT), full insert sequence.			
ACCESSION	AK018423.1	GI:12858114		
VERSION	AK018423.1			
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (strain:C57BL/6J) 16 days embryo lung cDNA to mRNA, clone:lib:RIKEN full-length enriched mouse cDNA library			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
PUBMED	99279253			
REFERENCE	10349636			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	2049374			
PUBMED	11042159			



Oy		541	TATGGAATTACAAATGGCAAAAACAATCCAAATCATCTTCAAGATGGGGCGTGTT	600
Db		713	TATGGAATTATAGGTGGCCAAAGCAGAACGATTCATCTTAAGSTGGAGCCATTCTG	772
Oy		601	GGTGGGGCTCTCTCTGTGGTGTGCAGTGTCTGTGTGTGTCTGTGGCAAAGATCTTGG	660
Db		773	GGTGGCATAGCTCTCTCTGTGGTGTGCAGATTACTGGCATAGTGTCTGTGGCAAAG--CTGG	829
Oy		661	AATTCAGACATCACCCCTTCTGACACATCAAGTTTCAATCTTCTCTTGAATTTGCCATTTCAAG	720
Db		830	AACACAGACGTACCTCTCTGTGTGCATCAGCTGCATTTTTCCCCTTGTGTGGCCATGTACACA	889
Oy		721	GGTTTTCGTGTGGCACTTTTACCACACAGCTTTGTGGCAAAGSTVGAGACAAATTTTCTTTA	780
Db		890	GGCTTCTCTGTGGCAATCTCTCAACCAACCAATTTTGGCAAAGSTGCAGAACCATTTTCCATA	949
Oy		781	GAATCTGAGCTCAGAAATATTTTCAGATGTGCATCACATGTCTTCAGTTATCTTTCACGTCT	840
Db		950	GAGAATGGCGCTCAGAAACATTCAGCTGTGTGCATGTGCATGTCTCAGCTGTCTCTCTGTCT	1000
Oy		841	GAGCACTGTGTCCAAATGTGTAGTTTCCCATCTGGCTTATGACCTCTTCCAGCTGATTAAT	900
Db		1010	GAGTACCTGTGCACACTGTCTAAACTTTGTGATTGTGGCTTATGACCTCTTCCAACTGTCTGAC	1065
Oy		901	GGATTTCTTATTTGTGTCAGACATATCAGACGTACAGAGAGAGATTGAAAGAACAAATGGA	960
Db		1070	GGCTGTCTCATTTGTGTGCAGCAATTCAGGCATTCAGAGAGGCAAGAGTAAATGTGCAG	1122
Oy		961	AAAAAGAACTCAGGTTGCA CAGAACTGTCTGCATTCAGAGAAATGCACTTCTTCCAGAGAG	1020
Db		1130	AGACAGCAACCCGAGTTGGCCCAACACGTCTGTCTACGAGAAACA-----GCCACAGAG	1180
Oy		1021	ACCAATGCGCTTCTGTGAGGTGAATTAAGAAAGSTGCATCACTCTCGGGCCACACAGGCGCA	1080
Db		1181	ACCAATGCTTTCTTTGATTAAGAGGAGTAGGCTGTCCGTACTCTGTGGGCGCATGTGCAGCCA	1240
Oy		1081	ATGATTTGCCACAGGGGCTCTCCAGCGAGTTGGCCACATCACTTCAATGTGCAATG	1134
Db		1241	GAGCAGCAACACAGGGGCTGTGAGCTGACTGACTACCACTTCTTCAATGTGCAATG	1294
RESULT 2				
LOCUS	BB613812	652 bp	mRNA	linear EST 26-OCT-2001
DEFINITION	BB613812 RIKEN full-length cDNA, 0 day neonate head Mus musculus			
VERSION	BB613812			
KEYWORDS	BB613812.1 GI:16454310			
SOURCE	EST.			
ORGANISM	house mouse. Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 652) Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., , Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Komno,H., Koude, , M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki, , D., Shibata,K., Shimigawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toyota,T., Muramatsu,M. and Hayashizaki,Y.			
TITLE	RIKEN Mouse ESTs from Hayashizaki,Y.			
JOURNAL	Unpublished (2001)			
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@sc.riken.go.jp/ URL:http://genome.gsc.riken.go.jp/			

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh  
M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagii, K., Fujimasa, S., Inoue, K., Togawa, Y., Irawa, M., Ohara, E.,  
Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,  
S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and  
Hayashizaki, Y.

Riken integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multichipillary sequencer. genome Res.  
10 (11), 1757-1771 (2000)

Komno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,  
Y. and Hayashizaki, Y

Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Kondo, S., Shingawa, A., Salto, T., Kiyoawar, H., Yamakita, I., Aizawa,  
K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and  
Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with  
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
further details.

e mouse tissues.

FEATURES

SOURCE

Location/Qualifiers

1..652

/organism="Mus musculus"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="4831431E11"

/clone\_lib="RIKEN full-length enriched, 0 day neonate  
head"

/sex="mixed"

/tissue\_type="head"

/dev\_stage="0 day neonate"

/lab\_host="DHI0B"

/note="Site\_1: Salt; Site\_2: BamH; cDNA library was  
prepared and sequenced in Mouse Genome Encyclopedia  
Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGGAGAAGATCCACGAAGCTCTTTTGTGGTTTTTTVN 3'] . cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. cDNA went through one round of normalization  
to Rot = 10.0 and subtraction to Rot = 100.0. Second  
strand cDNA was prepared with the primer adapter of  
sequence [5' GAGGAGAAGATTTCGAGTAATAAATTAATCCCCCCCCCC  
3']. cDNA was cloned into the XhoI and BamH sites.  
Vector: a modified Bluescript KS(+) after bulk excision  
from Lambda PLG I."

BASE COUNT

118 a 172 c 173 g 189 t

ORIGIN

Query Match 39.7%; Score 450.4; DB 10; Length 652;  
Best Local Similarity 81.7%; Pred. No. 2.8e-119;

Matches 533; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

Oy AGCTCGTTTGACAAGTAGTGCACATGATGATGGGGCTCATATGTCCTTTGGAT 151  
Db AGTGCTTTTAAAGTAGTGTCTCGACTGATGATGGGTTGGTCAATGTTCTTTGGAT 63

Oy GTTCCGTRGAGATGCCGAAGCTGTGTGTGCACATCAAGAACCCCTGGGGCATTTGCTG 211  
Db GTTCTGRGAAGTCAGAAAGCTGTGTGTGCACCACAAAAGCCCCTGGGGCATGCCAGTG 123

Oy GACTGCTGTGCAGTTTGGGCTCATGCTTTTACAGCTTATCTCTGGCCATTAAGCTTT 271  
Db GCCTGCTTTCACATTGGACTTATGCTCTGAAGAGCTTATCTGTAGCACATTGGCTTGG 183

Oy	272	CTCTAAGGCACTCCAAAGCTATTGCTGTCTCATCAATGGAGCTGCTCCGAGGGGAGCA	331
Db	184	GCTGAAACCAATCCAAAGCTATTGCTGTCTCATATAGGGAGCTCCTCGGGGAGCA	243
Oy	332	TCTCTAACATTTTCACTTTCTGGGTGATGAGATATGAGATCTCAGCATCATATATACA	391
Db	244	TCTCTAAATGTTCTCACTTTCTGGGTGATGAGATATGAGATCTCAGCATCATATATACA	303
Oy	352	CCTGTTCACCGTGGCGCGCTGGGAATATGCACTGCACTTATCTCTACCTGGT	451
Db	304	CTGTGTTCAAGAGGCGCGCTGGGAATATGCTCTGTGCTCTACATTTACACCGGT	363
Oy	452	CTTGAGTCTTCAGCAGAACTCACCATTCCTTATCAGAACATAGAAATTAACCTTGTGT	511
Db	364	CCTGAGCTCTGCACAGAACTGTGATTCCTGATCAGAGCATAGAAATTAACCTTGTGT	423
Oy	512	GCCTAGCACTTCTGTGTGCTTGTGTGTCTATATGAAATTAACAGATGGCCAAAACAATCCA	571
Db	424	CCCTGTGTGTTCTGTGTGCTTCTGTGTGTCTATATGAAATTAAGTGTGCCAAAAGCAA	483
Oy	572	AAATCATTTCTCAAGATTGGGGCGGTGTGTGTGGGTCTCCTCTGTGTGTGTGCAGTTG	631
Db	444	CGGTATTTCTAAAGTGTGAGAGCCATTTCTGGGTGTGATGCTCTCTGTGTGTGTGTGAGTTA	543
Oy	632	CTGTGTGTGTCTGTGGGAAAGATCTTGGAATTCAGACATCACCTTTGACCATCAGTT	691
Db	544	CTGGCATGTGCTGTGGGAAAG---CTGGAACACAGACGTCACTTTCTGTGTGTGTGAGCT	600
Oy	652	TCATCTTTCTTGATATGGGCAATGACAGGGTTTTGTGTGTGTGTGACATTTTAC	743
Db	601	GCATTTTCTCCCTGTGTGTGGCAATGTACAGGCTCTCTGTGTGTGTGTGTGTAC	652

RESULT 3					
LOCUS	BG872314				
DEFINITION	60219097771 NCI_CGAP_SG2 Mus musculus cDNA clone IMAGE:4922227 5', mRNA sequence.	972 bp	mRNA	linear	EST 29-MAY-2001

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE 1 (bases 1 to 972)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: [CSapbs-10@mail.nih.gov](mailto:CSapbs-10@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: LRAM10841 row: j column: 20  
High quality sequence stop: 786.

**FEATURES**  
**source**

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source
1..972
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4922227"
/clone_1ib="NCI_CGAP_SG2"
/lab_host="DH10B (T1 phage-resistant)"
/notice="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1:
Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      222 a      277 c      263 g      210 t

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## ORIGIN

Query Match	29.6%;	Score 335.4;	DB 12;	Length 972;
Best Local Similarity	73.8%;	Pred. No. 6.9e-86;		
Matches 458;	Conservative 0;	Mismatches 151;	Indels 12;	Gaps 2

QY	514	TTGACAAATTCCTGTGGCTTCTTGTTGTCTATGTGAATTAACAGATGGCCAAACATTCGAA	573
Db	1	CTGGTGGTCTCTGTGGCTTCTGGCGCTATGTGAATTAATAGTGGCCAAAGCAAGCAACG	60
QY	574	ATCATCTCAAGATTGGGGCCGTGTGGTGGTGGGGTCCCTCTTCTGTGGTGGCAGTTGCT	633
Db	61	GTATTTCTCAAGTGTGGAGCATCTTGGGTGGCATGTCCCTCGTGGTGGTGGCAGTTACT	120
QY	634	GGTGTGCTCTGGCGAAAGAGATCTTGGAAATTCAGACATCACCTCTTGCACATCAGTTTC	693
Db	121	GGCATGTGCTCCGGCAAAAG---CTGGAACAACAACGTCATCTTCTGGTATCAGCTGC	177
QY	694	ATCTTTCCTTTGATTGGCAATGTGACGGGGTTTTGTGCTGGCAGCTTTTATCCACCAAGCT	753
Db	178	ATTTTCCCTTGTGTGGCATGTACAGAGCTTCTGTGGCATTTCTCACCCACCAATCT	237
QY	754	TGGCAAGGTGTCAGAGACAAATTTCTTGAACAACTGAGGTCAAGATATTCAGATGTGATC	813
Db	238	TGGCAAGGTGTCAGAGACAAATTTCTTGAAGACTGGCGCTCAGAACATTCACCTGTGCATC	297
QY	814	ACCATGCTCCAGTTATCTTTTCACTGTCTGAGACATTTGGTCCAGAGTTGAATTTCCCACTG	873
Db	298	GCCATGTGCAAGCTGTCTCTTCTGTGTGAGTACCTGTGTCAGCTTAACTTTTGCATTG	357
QY	874	GCCATGTGACTCTTCCAGCTGATGATGAGATTTCTTATTTGTGAGCATATCAGACGTAC	933
Db	358	GCCATGTGACTCTTCCAGTGTCTCAGCGGTGTCTATTTGTGCGACGATATCAGGCAATAC	417
QY	934	AAGAGAGATTTGAAGAACAAACATGAAAAAAGAACTCAGTTGCAAGAACTCTGCCAT	993
Db	418	AAGAGAGAGCGAAGAGATTAATGCAGGAGACAGCACCGGATTTCCAGAGAGTCTGCAC	477
QY	994	ACGAGAGAAATGACTTCTTCCAGAGAGACCAATGCTCTTCTGAGAGTGAATGAAGAAAGT	1053
Db	478	GAGAAAGCA-----GCCAGAGAGACCAAGTCTTTCTTGGATTAAGGGGATGAGGCT	528
QY	1054	GCCATCACTCTGGGCGAACAGGGCCCAATGAGATTGCACAGGGCTCTTGAGCCAGTTGGC	1113
Db	529	GCCGTAATCTGTGGGCGCAGTGCACACCAAGAGACACACAGGGCTGTGAAGTCACTAGC	588
QY	1114	CACATCACTTATGTGAATAG 1134	
Db	589	CACATTCCTTCATGTGAATAG 609	

RESULT		4
BEI81226		
LOCUS		
DEFINITION	BEI81226	356 bp mRNA linear EST J2971-2000
ACCESSION	CW-000630-220300-125-F05 HT0630	Homo sapiens CDNA, mRNA sequence.
VERSION	BEI81226	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	

REFERENCE  
AUTHORS  
1 (bases 1 to 356)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
MEDLINE 20202663







QY	241	TTTAAAGCTTATCTCTCTGCGCATTAAGCTTTTCTCGAAGCCAGCAGTCATGCTGTT	300
DB	259	GTGACAGGTTAAACAGAAACCGATTGCGCTGATGGGTTGAACATTCACAGCTGTTATGTC	318
QY	301	CTCATCATGAGGCTGCTGCGCCCGGGGGGACACATCTCTAAATTTTCACTTCGAGTTGAT	360
DB	319	CAAAATGATGGGGAGCGCTGCGCTGGGGGACACATGTTGAAGGTCGTAACCTTGCGGGTTGA	378
QY	361	GGAGATATGATCTCA	376
DB	379	GGAGATATGATCTCA	394
RESULT 7			
AU176916			
LOCUS			
DEFINITION	AU176916	642 bp	mRNA
	AU176916	Sugano-Kawakami 5' end enriched cDNA library (Ola)	EST 21-MAR-2001
		HNI Oryzias latipes cDNA clone Ola22.10c similar to p1r1A498761	
		Na+-dependent bile acid transporter, 11a1 - golden hamster, mRNA	
sequence.			
ACCESSION	AU176916		
VERSION	AU176916.1	GI:13425752	
KEYWORDS	EST.		
SOURCE	Japanese medaka.		
ORGANISM	Oryzias latipes.		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
	Acanthomorphi; Acanthopterygii; Percomorphi; Atherinomorpha;		
	Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.		
	1 (bases 1 to 642)		
REFERENCE	Narusue, K., Mitani, H. and Tanaka, M.		
AUTHORS	Medaka EST Project in University of Tokyo (2001)		
TITLE	Unpublished (2001)		
JOURNAL	Contact: Kiyoshi Narusue		
COMMENT	Department of Biological Sciences		
	Graduate School of Science, University of Tokyo		
	Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan		
	Tel: 81-3-5841-4443		
	Fax: 81-3-5841-4410		
	Email: narusuebio1.s.u-tokyo.ac.jp		
	This clone was isolated from Sugano-Kawakami 5' end enriched cDNA		
	library (Ola).		
FEATURES			
source	1..642	Location/Qualifiers	
	/organism="Oryzias latipes"		
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	(Ola) From HNI"		
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BASE COUNT	106 a	200 c	167 g
ORIGIN			169 t
Query Match	17.1%	Score 194.2	DB 9; Length 642;
Best Local Similarity	66.7%	Pred. No. 5	1e-45;
Matches	277; Conservative	0; Mismatches	138; Indels
		0; Gaps	0
QY	109	GTGTCCATCTGTGATGATGGGCGCTGCTCATGTTCTTTGGATGTTCCGTGGAGATCCGG	168
DB	228	GTGTCCATCTGTGATGCTGCGCCATGATGTCATGTTCCGATGGCTGCACGGTGGACCTTCGG	287
QY	169	AAGCTGTGTGGCACAATCAGAGAGACCCCTGGGGCATTCGCTGTGGAGACTGCTTGCACAGTTT	228
DB	288	AAGCTGTGGGTCACATCAGAGACCTTGGGGCATTCGTCATGGCTTCAATCTGCCAGATT	347
QY	229	GGGCTCATGCTTTTACAGACTTATCTCTGGGCATTTAGCTTTTCTCTGAAGCCAGATCCAA	288
DB	348	GGCATCATGCCCTTACAGGCGCTTCGGCGCTGCTCCCTTCGCTTCAAGCTTCTGCTGTGACG	407
QY	289	GCTATTGCTGTTCTCATCATGAGCGCTGCTGCCCGGGGGGACACATCTTAAATTTTAC	348

Db	408	GCATCGTCATCATCATCATGAGTTGCTGTCCTTGAGAGCTTCAGCTCCACATCATCTGT	467
Qy	349	TTCTGGGTTGATGAGATATGATGATTCAGCATCAGTATGACAACTGTTCACCGGTGACC	408
Db	468	TACTGGCTGATGAGACATGACATGACCTGAGCATCAGTATGACGAGCTGTTCCTCATCTGT	527
Qy	409	GCCTGGGAATGATGCCACTTCTGCATTTATCTTACACCTGTGCTCTGAGCTTCAGCAG	468
Db	528	GCCCTGGGAGATGAGCCCTCTGCTGCTTCACTTACACCAACGCTGTGACCTCAGCGAC	587
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Db	588	TCTATCATGATCCCTTTGACAGCATCGCATCCGCTGCGCCGCTTGTCTATCC	642
RESULT 8			
LOCUS	BI768670	760 bp	mRNA linear EST 25-SEP-2001
DEFINITION	603057222P1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5206781 5',		
ACCESSION	BI768670		
VERSION	BI768670.1	GI:15760248	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 760)		
JOURNAL	NIH-MGC http://mgs.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs-rcmail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:		
	http://image.llnl.gov		
	Plate: L14M1518 row: k column: 06		
FEATURES	High quality sequence stop: 760.		
source	Location/Qualifiers		
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	/clone="IMAGE:5206781"		
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	/lab_host="DH10B"		
	/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung; 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note this is a NIH_MGC Library."		
BASE COUNT	181 a 185 c 190 g 204 t		
ORIGIN			
Query Match	16.7%; Score 189; DB 13; Length 760;		
Best Local Similarity	62.9%; Pred. No. 1.7e-43;		
Matches	325; Conservative 0; Mismatches 190; Indels 2; Gaps 2		
Qy	80	ATGGAACCTGAGACTCGTTTTCACAGTGTCCATCTGATGATGAGGCGGTCTCATGT	139
Db	245	ATAACATCTTAAGTGTGCTCTAAGTACGGGTGACCATCTGTGGCTTGGATGT	304
Qy	140	TCTCTTGGATGTTCCTGTGAGATCCGGAAGCTGTGTGGCACATCAGAGACCTCTGG	199

Db 305 TCTCCATGGAGTCAACGTGGAAATTCATAGAAATTTCTAGGGCAGCATTAACGGCCCTGGG 364

Qy 200 GCATTCCTGTGGAGTCTCTGCGCAGTTGGGCTCATAGCTTTTACAGCTTATCTCTGG 259

Db 365 GCATTTGTGTGGCTTCTCTGTCATTTGGATCATAGCCCTCACAGAGTTATCTCTGT 424

Qy 260 CCATTAGCTTTTCTCTGAAAGCCAGTCCAAAGCTTATGCTTTCTCATCATGAGGCTGCTGCC 319

Db 425 CGGTGGCTTTTGTGACATCTCCCTCCAGGCGCTAGTGGTGCCTATTATAGAGTGTCTGCC 484

Qy 320 CGGGGGGGCCCATCTCTATACATTTTCACTTCTGGGTGATGAGATATGAGATCTCAGCA 379

Db 485 CTGGAGAACTGCTTCCATATTTTGGCTTATTTGGTTCATGAGCAGATGAGACCTTGAAG 544

Qy 380 TCAGTATGACAACTGTTCCACCGTGGCCGCTGGGAAATGATGACCACTCTGCAATTATC 439

Db 545 TACAGTACGACATGCTCCACAGCTGCTGGGAAATGATGCGGCTGTGCTCTTGA 604

Qy 440 TCTACACCTGTGCTCTGAGTCTTACAGACATCTCACATCTCTTATACAGACATGAA 499

Db 605 TCTATACCAAAATGTGGGTGAGCTGTGGAGCATCTGAATTCCTATATGATTAACATAGTA 664

Qy 500 TTACCTGTGTGCTGACCATCTCTGAGCTTTGGTGTCTATGATTAACATAGTGC 559

Db 665 CATCTCTGAGTCTCTGCTTGTCTGTTTCTCATTTGGAATGT-TGTTAATCAGAAATGCG 723

Qy 560 CAAACATCCAAATCATTTCTCAAGATTGGGCGGT 596

Db 724 CCAAA-AAGCAAGATCATCTTAATAATTGGTCCAT 759

RESULT 9  
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LOCUS CM2-HT0285-081199-028-a09 HT0285 Homo sapiens cDNA, mRNA sequence.  
DEFINITION BE151388  
ACCESSION BE151388.1 GI:8614109  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 274)  
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
COMMENT Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the PABSP/LIKR Human Cancer Genome Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=<t2=CM2-HT0285-081199-028-a09&t3=1999-11-08&t4=1)  
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BASE COUNT 82 a 71 c 71 g 50 t  
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Query Match 16.2%; Score 184; DB 10; Length 274;  
Best Local Similarity 96.8%; Pred. No. 3.5e-42;  
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Qy 164 TCCGAGAGCTGTGTGACATCAGAGACCTGGGGAGTTGCTGGAGTCTGTGCC 223  
Db 272 TACGGAATCCGTTTCCGACATCAGAGACCTGGGGCATTTGCTGGAGTCTGTGCC 213  
Qy 224 AG-TTTGGGCTCATGCTTTTACAGCTTATCTCTGGCCATTAGCTTTTCTGAAAGCA 282  
Db 212 AGTTTGGGCTCATGCTTTTACAGCTTATCTCTGGCCATTAGCTTTTCTGAAAGCA 153  
Qy 283 GTCCAGCATATGCTGTTCTCATCATGAGGCTGTGCC-CCGGGGGGCACCATCTTAACAT 341  
Db 152 GTCCAGCATATGCTGTTCTCATCATGAGGCTGTGCCCTGGGGGGCACCATCTTAACAT 93  
Qy 342 TTTCACTTCTGGGTTGATGAGATATGAGATCTCAG 377  
Db 92 TTTCACTTCTGGGTTGATGAGATATGAGATCTCAG 57

RESULT 10  
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LOCUS RPI11-2407.TKBF RPCI-11 Homo sapiens genomic clone RPCI-11-2407,  
DEFINITION AQ013853  
ACCESSION AQ013853.1 GI:3186418  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 543)  
Adams,M.D., Rounsailey,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., BERRY,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.  
Use of BAC End Sequences for Sequence-Ready Map Building (1998)  
Unpublished (1998)  
COMMENT Other\_GSSes: RPI11-2407.TKBF  
Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mcdams@tigr.org  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/cdb/hunguen/bac\_end\_search/bac\_end\_search.html  
Class: BAC ends.  
Location/Qualifiers  
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/clone="RPCI-11-2407"  
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/sex="Male"

## FEATURES

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	QY	260	CCATTAGCTTTTCTCTGTAAGCCAGTTCACAGCTAATTGCTGTCTCATCATGGGCTGCTGCC	319		
	Dd	365	CTGTGGCCCTGTGGCAATCCTTCTCTGTACAGGCGTGTAGTGCTTAATTATGAGGTTCTGTGCC	424		
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	Dd	425	CTGGAGGAACCTGGCTCCCAATATCTCTGGCCTTATTTGATGATGCGCATTTGGACCTCAGTG	484		
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	VERSION	Bt149148.1	GI:14609149			
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	ORGANISM	Mus musculus				
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		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
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	REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.				
	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)				
	TITLE	Unpublished (1999)				
	JOURNAL	Contact: Robert Strusberg, Ph.D.				
	COMMENT	Email: cga@bs-remail.nih.gov				
		Tissue Procurement: Jeffrey E. Green, M.D.				
		CNA Library Preparation: Life Technologies, Inc.				
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)				
		DNA Sequencing by: Incyte Genomics, Inc.				
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:				
		http://image.llnl.gov				
		Plate: LLM1145 row: k column: 19				
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		/lab_host="DHIOB (TI phage-resistant)"				
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Db		292	GCATCATCTTGGAAAGCCCAAAGGGGGATCATGCGCATAGTAGGCCAGTACGGTATCATG	351
Oy		238	CCTTTTACAGTATATCTCTCGGCGCATTAAGCTTTTCTCTGAAGCCAGTCCAAAGCTATTGCT	297
Db		352	CCCCCTCAGTCTTCCCTTCTGGGGCAAGGCTTTTCATCTGACACAGCATTTGAGGCTCTGGCC	411
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Oy		358	GATGAGATATGATATCTCACATCATAGTATGACAACCTGTTCACCGTGGCCGCGCTGGGA	417
Db		472	AAGGGGACATGAACCTCAGATATTGATGACCACTGCTCAGCTTCACCTTCAGCTTGGGCG	531
Oy		418	ATGATGCCACTCTGCAATTTATCTTAACT--GTTCTGGAAGTCTTCAGCAAAATCTC	474
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Oy		475	ACCATTCCTTATCAGAACATAGAAATTAACCTTGTTGGCCGACCATTTCTGTGGGCTTT	534
Db		592	AAGGTGCCCTTACAAAGGCATTAATGTTATCACTGTCATGTTCTCATCTCTTGGCCATA	651
Oy		535	GGTGTCTATGTAATTCAGATGGCCAAAACATCCAAAATCATCTTCAGATTGGGGCC	594
Db		652	GGGATCTTCCGAAGTCCAAAAGGCCACACATATTAACCTTACGCTCAAGGAGCGATG	711
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Db		712	ATCATCACTTCTCTCTCTCTGTGGCTGTACAGT	746
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DEFINITION		60202855F1 NCI_CGAP_Li9	Mus musculus cDNA clone IMAGE:4163893 5'	
VERSION		BP234728		
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SOURCE		EST.		
ORGANISM		house mouse.		
REFERENCE		Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE		NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL		National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT		Unpublished (1999) Contact: Robert Straubeberg, Ph.D. Email: cgabos-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNU) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNU at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM9448 row: m column: 14 High quality sequence stop: 684. location/Qualifiers 1..876 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:4163893" /clone_lib="NCI CGAP Li9" /lab_host="DH10B (TI phase-resistant)" /note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.		
FEATURES				
source				

Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library.  
BASE COUNT 190 a 265 c 222 g 198 t 1 others  
ORIGIN

Query Match 12.5%; Score 141.2; DB 12; Length 876;  
Best Local Similarity 55.9%; Pred. No. 1.3e-29;  
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QY 178 TCGACATAGAGAGACCTGGGCAATGCTGTGGGACTGCTGACGATTGGGCTCATG 237
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Db 243 GCTCATCTTCTGAGAGCCCAAGGGGTGATCATGCGCATAGTGGCCGACGATACGGTATCATG 302
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Db 423 AAGGGGACATGAACTCAGCATGTGATGACCACCTGCTCCAGCTTCACTGCTTGGGC 482
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QY 418 ATGATGCCACTCTGCATTTATCTCTACACT---GGTCTGAGTCTTACGAGATCTC 474
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